

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: June 29, 2002, 22:09:00 ; Search time 17398.4 Seconds
(without alignments)
693.528 Million cell updates/sec

Title: US-09-303-518D-571

Perfect score: 894
Sequence: 1 atgttcgttaccatcag.....accgctaaacgcgctaa 894

Scoring table:

IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 13736207 segs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

EST:*
1: em_estha:*
2: em_esthm:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hic:*
9: gb_est1:*
10: gb_est2:*
11: gb_hic:*
12: gb_gss:*
13: em_gss_hum:*
14: em_gss_inv:*
15: em_gss_pln:*
16: em_gss_vrt:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	42	4.7	513 12	PI91L
2	41.8	4.7	727 10	BI805731
3	41.6	4.7	1101 12	CNS0175Y
4	40.8	4.6	910 12	CNS0060N
5	40.6	4.5	839 12	CNS0044B
6	40	4.5	427 9	AI380814
7	40	4.5	448 9	AI176455
8	40	4.5	454 9	AI1016947
9	40	4.5	489 10	BF940160
10	40	4.5	530 10	BF115042
11	40	4.5	596 9	AI219883
12	40	4.5	622 9	AI806391
13	40	4.5	1101 12	CNS00KK2
14	39.8	4.5	643 9	BB620231
15	39.8	4.5	643 9	BB657008
16	39.8	4.5	653 10	BI960503
17	39.8	4.5	685 9	BB645508
18	39.8	4.5	1100 12	CNS016KD
19	39.6	4.4	925 12	CNS0091P
20	39.2	4.4	542 10	BI724201
21	39	4.4	421 10	BI952636
22	39	4.4	627 9	AI825645
23	38.8	4.3	658 12	AQ397507
24	38.6	4.3	452 10	BF839785
25	38.6	4.3	494 10	BE461007
26	38.6	4.3	502 10	BE471037
27	38.6	4.3	545 10	BG904253
28	38.6	4.3	1159 12	CNS015XR
29	38.4	4.3	318 9	AM083767
30	38.4	4.3	487 9	AM386998
31	38.4	4.3	498 9	AM594194
32	38.4	4.3	546 9	AM237064
33	38.4	4.3	551 9	AI989498
34	38.4	4.3	588 10	BE463918
35	38.4	4.3	725 10	BI517775
36	38.2	4.3	406 10	BI723631
37	38.2	4.3	499 10	BI723630
38	38.2	4.3	535 10	BI724519
39	38.2	4.3	604 10	BI723629
40	38.2	4.3	633 10	BG907322
41	38.2	4.3	639 10	BI717021
42	38.2	4.3	686 10	BG909263
43	38.2	4.3	822 10	BI990087
44	38.2	4.3	1101 9	AL513871
45	38	4.3	535 10	BI531370
46	38	4.3	703 10	BI917026
47	38	4.3	998 12	CNS0306L
48	37.8	4.2	692 12	CNS007WH
49	37.8	4.2	1092 10	BE418041
50	37.8	4.2	1101 12	CNS0178
51	37.6	4.2	527 9	AV623739
52	37.6	4.2	665 10	BG854378
53	37.6	4.2	666 10	BG854379
54	37.4	4.2	1039 12	CNS006H7
55	37.2	4.2	973 10	BE103899
56	37	4.1	536 10	BE596708
57	37	4.1	600 9	AI403544
58	37	4.1	645 12	CNS01213
59	37	4.1	842 12	CNS023AR
60	37	4.1	1101 12	CNS012S8
61	37	4.1	1200 10	BE427234
62	36.8	4.1	352 9	AI917857
63	36.8	4.1	471 9	AI184528
64	36.8	4.1	484 9	AI218896
65	36.8	4.1	547 9	AI215072
66	36.8	4.1	614 9	AI741885
67	36.6	4.1	369 9	AL503995
68	36.6	4.1	374 10	BF421930
69	36.6	4.1	540 9	AA475527
70	36.6	4.1	751 10	BF866626
71	36.6	4.1	1101 12	CNS007SC
72	36.4	4.1	420 12	BE611073
73	36.4	4.1	585 10	BM000392
74	36.2	4.0	312 10	BM286054
75	36.2	4.0	480 10	BE681679
76	36.2	4.0	844 12	CNS0052P
77	36	4.0	482 10	C06823
78	36	4.0	604 9	AUI35015
79	36	4.0	614 12	AQ082014
80	36	4.0	723 9	AUI32443
81	36	4.0	850 10	BF577545
82	36	4.0	972 12	CNS002JY
83	35.8	4.0	430 10	BG047727
84	35.8	4.0	455 12	AZ132296
85	35.8	4.0	507 10	BE599418
86	35.8	4.0	547 9	AM922793
87	35.8	4.0	655 10	BM379814
88	35.8	4.0	665 10	BI524115
89	35.8	4.0	792 10	BG342884
90	35.8	4.0	916 12	CNS013P9
91	35.8	4.0	916 12	CNS013P9
92	35.8	4.0	916 12	CNS013P9
93	35.8	4.0	916 12	CNS013P9
94	35.8	4.0	916 12	CNS013P9
95	35.8	4.0	916 12	CNS013P9
96	35.8	4.0	916 12	CNS013P9
97	35.8	4.0	916 12	CNS013P9
98	35.8	4.0	916 12	CNS013P9
99	35.8	4.0	916 12	CNS013P9
100	35.8	4.0	916 12	CNS013P9

C	91	92	93	94	95	96	97	98	99	100
	35.8	4.0	994	12	CNS0303UN	AL261536	Tetraodon			
	32.8	4.0	1101	12	CNS0161M	AL106910	Drosophila			
	33.8	4.0	1815	11	AK014308	AK014308	muscu			
	33.6	4.0	563	10	B1975596	B1975596	484611	MA		
	35.6	4.0	619	10	BE360374	BE360374	DGI_63_F0			
	35.6	4.0	627	10	B1873923	963112B09	B1873923	HVSMEN001		
	35.6	4.0	665	10	B1959301	B1959301	HVSMEN001	HVSMEN001		
	35.6	4.0	680	10	B1959500	B1959500	HVSMEN001			
	35.6	4.0	846	12	CNS010RT	AL099337	Drosophila			
	4.0	961	10	EG024840	BG024840	602275583				

ALIGNMENTS

Db	299	GTCACCGAGGACAC	312
RESULT	2		
BI805731			
LOCUS			
DEFINITION		727 bp	mRNA linear
			EST 02-OCT-2001
			Oryza
			S043H12 Stem library from Oryza sativa (3-5 leaf stage)
			Oryza
			sativa cDNA clone S043H12, mRNA sequence.
ACCESSION			
VERSION			
			BI805731
			BI805731.1
			GI:15852935
KEYWORDS			
SOURCE			
			EST.
			Oryza sativa.
ORGANISM			
			Oryza sativa.
			Stratocaulon: Embryophyta: Tracheophyta;

LOCUS	DEFINITION	RESULT 1
P191L	513 bp DNA	GSS 17-MAR-2000
P191L	Leishmania major Friedlin PAC P191 left end sequence, similar to SM:HRB.ECOLI P24187 LIPID A BIOSYNTHESIS LAUROYL. . . N-158, Prob-8.8e-24, genomic survey sequence.	

ACCESSION	AL161299	GI:7271280
VERSION	AL161299.1	
KEYWORDS	GSS.	
SOURCE	Leishmania major.	
ORGANISM	Leishmania major	

REFERENCE AUTHORS	1 (bases 1 to 513)
Ivens, A. C., Lewis, S. M., Bagherzadeh, A., Zhang, L., Chan, H. M. and	

TITLE	Smith, D. E.
JOURNAL	A physical map of the Leishmania major Friedlin genome
MEDLINE	Genome Res. 8 (2), 135-145 (1998)
REFERENCE	98146435
AUTHORS	2 (bases 1 to 513)
	Taylor, R.G., Huckle, E.E.J., Ivens, A.C., Rajandream, M.A. and

TITLE Direct Submission
JOURNAL Submitted (12-MAR-2000)
Leishmania major Friedlin genome sequencing
Submitted 12-MAR-2000
Author Friedlin, Robert C. & Hinton, David R. & Trust, Cecelia & Campese, William J. & ...

COMMENT
see <http://www.ebi.ac.uk/parasites/leish.html>
Details of Leishmania sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/projects/L_maj/
The primer sequence can be obtained from alicat@sanger.ac.uk.

FEATURES	Location/Qualifiers
source	1. 513

SOURCE	BASE COUNT	ORIGIN
/organism="Heliobacterium majus"	91 a	181 c
/strain="Friedlin"	157 g	83 t
/db_xref="taxon:5664"		
/clone="PAC P191"		
		1 others

Query Match	4.73;	Score 42;	DB 12;	length 513;
Best Local Similarity	51.08;	Pred. No. 1.1;		
Matches 99; Conservative	0;	Mismatches 95;	Indels 0;	Gaps 0.

Qy 616 gaagcggcggcgtgtygcgatlttttcggcaaacctycatacaccaatgaacactgccc 675
|| ||| | | | | | | | | | | | | |
Db 119 GAGCCGACATCCGAGCTTCGTGCCCTTCTTTGGCGCCGCCAGCGCGCTGACGCTTGACTTCGGTA 178

Oy	676	gcaaaattggcacacgcgtcaaaagcgctgaanaaccctgttttctcgtcgcgaacgcctgcc	735
Db	179	TGCGGCTGGCGGCGGTACCGGCGCAAGCTGTGCCGATCTATTACGAGCAGCTGCC	238

Oy		736	gacgcacaagcgttcgttgtcacatcgccccgtccaaagggaattgaacygcaacaaa	795
Db	239	GACATATCGGCTATGTGCTCCGGATCCTGCCAGCCTTGGGACAACATA	TCCGGGGCGAGAAC	298

QY 796 gccacgatgccgc 809

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
1 (bases 1 to 727)	Dong,H.T., Li,D.B., Zhuang,X.F., Dai,C.G., Sun,L.X., Pei,Y.X., Wu,H.F., Jiang,Y.X., Yu,P.C., Gao,Q.K. and Lou,Y.C.	A Gene Expression Screen in <i>Oryza sativa</i>	Unpublished (2001)	
Contract: Dong HT	Laboratory of Functional Genetics	Bio-technology Institute of Zhejiang University	Kaixuan Road 268#, Hangzhou, Zhejiang, P.R.China	Tel.: 0086-571-86892051 Fax: 0086-571-86961525 Email: htdong@zjuem.zju.edu.cn Seq primer: M13 forward primer.
FEATURES	source	Location/Qualifiers		
	1..727	/organism="Oryza sativa"		
	/db_xref="taxon:4530"	/clone="S043H12"		
	/clone_lib="Stem library from <i>Oryza sativa</i> (3-5 leaf stages)"	/tissue_type="Stem"		
	/dev_stage="3-5 leaf stage"	/note="Vector: pSPORT2"		
BASE COUNT	145 a	257 c	209 g	116 t
ORIGIN				

Query Match	4.7%	Score 41.8;	DB 10;	Length 727;
Similarity	45.7%	Pred. No. 1.4;		
Best Local				
Matches 145;	Conservative	0;	Mismatches 172;	Indels 0;
				Gaps 0;

128 gacatctgcgttcttacccttctaagaagacccgcgcgcacatcgttcgccaatatgcgc 187

Db 114 GATCTCAAGGGGCTTCGCCGCGACGAAAGGAGCGCACCATGGCCCAAGCTCCACG 173

QY 188 aggcgggtttgaaacccgcacgcagacgctcaaaagccgttttcgcgaaacgycnaat 247

Db 174 AGGCGTAAAGGACTGGGGCTTCTCTGGGTGAAACCATGGCGTGGAGCGGCTTAA 233

248 gcggttgcactgccccggttttcaaaaaacggaagacatcgaaacaatgttca 307

Db 234 TGGAGCAGGTGAAGAGCTTCGTACCGGCATTTACGACGAGCACCCTGGAGAGAAATTCT 293

308 aaagcgtatcacgcgcctgaggaaacacgtgcagcagcgtcttgacaaagcgaagcgctgctgt 367

Db 294 ACGCCTCGACCTGCGCAAGAACCTCCACCTGAAACAAGACGACGGCGACGTCCTCGTCG 353

368 tcatcaagccgcacatcgcagctacgatttggcgcgcgcgtacatcagccagcagcttc 427

Db 354 ACGGGCGGACCTCGCCGACACAGCCGACTGGAGGCCACTACTTCATCCAGCACCGCC 413

0v 428 ccttcacctaacccgc 444

414 CCAAGAACCGCGCGCC 430

100

RESULT 3
 LOCUS CNS0175Y 1101 bp DNA linear GSS 26-JUL-1999
 DEFINITION Drosophila melanogaster genome survey sequence Sp6 end of BAC
 BACN37108 of Drosophila library from Drosophila melanogaster (fruit
 fly), genomic survey sequence.
 ACCESSION AL108460
 VERSION AL108460.1 GI:5628764
 KEYWORDS GSS.
 SOURCE fruit fly.
 ORGANISM Drosophila melanogaster
 Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
 Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
 REFERENCE 1 (bases 1 to 1101)
 AUTHORS Genoscope.
 TITLE Direct Submission
 JOURNAL Submitted (23-JUN-1999) Genoscope - Centre National de Sequencage ;
 BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
 - Web : www.genoscope.cns.fr)
 COMMENT Determination of this BAC-end sequence was carried out as part of a
 collaboration with the European Drosophila Genome Project (BDGP) -
 http://www.edgp.ebi.ac.uk/. This Drosophila melanogaster BAC
 library (Dros BAC) was made by Alain Billaud at CPH (Centre
 d'Etude du Polymorphisme Humain) with funding provided by a MRC
 project grant. The DNA was prepared from embryos by Alain Bucheton
 and Genevieve Payan. It has been constructed in the vector
 pBeloBAC11.
 FEATURES
 source Location/Qualifiers
 1..1101
 /organism="Drosophila melanogaster"
 /plasmid="pBeloBAC11"
 /db_xref="taxon:7227"
 /clone_lib="DrosBAC"
 /clone="BACN37108"
 /note="end : SP6"
 BASE COUNT 254 a 176 c 160 g 152 t 359 others
 ORIGIN
 Query Match 4.7%; Score 41.6; DB 12; Length 1101;
 Best Local Similarity 12.7%; Pred. No. 1.9;
 Matches 35; Conservative 140; Mismatches 101; Indels 0; Gaps 0;
 QY 329 acgtgcagcagcttgacgaaggcagcgtctgttcatacgcgcgcacatcgca 388
 ||:::|||||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
 Db 782 ACSSASGSSASGCGVSSGSSASGCGGCGGSSAVSASASASVMSKVASAVASCAVA 841
 QY 389 gctacgattggcgcgcgcacatcagcagcagcgttcgttcacacgcgcacatgt 448
 ||:::|||||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
 Db 842 SGMSAGAVSSSCRSVASVSAASVSSSSSSSSSSSSSSSSSSSSSSSSSSSSSS 901
 QY 449 acaagccgcgcaaatcaagcgaatagcaaatatcatcagcgcgcgcgcgcgcgcgc 508
 ||:::|||||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
 Db 902 AAAYAVSVSVSVSVSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSVTSSASVS 961
 QY 509 aagcgaacacgc 568
 ||:::|||||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
 Db 962 VSAVMSAVSVSS 1021
 QY 569 cggcgcgcgcacacatcatcctgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 604
 ||:::|||||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
 Db 1022 SSASSSV 1057
 RESULT 4
 LOCUS CNS0060N 910 bp DNA linear GSS 03-JUN-1999
 DEFINITION Drosophila melanogaster genome survey sequence T7 end of BAC #
 BACR14J71 of RPCI-98 library from Drosophila melanogaster (fruit
 fly), genomic survey sequence.
 ACCESSION AL065629
 VERSION AL065629.1 GI:4944698

KEYWORDS GSS.
 SOURCE fruit fly.
 ORGANISM Drosophila melanogaster
 Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
 Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
 REFERENCE 1 (bases 1 to 910)
 AUTHORS Genoscope.
 TITLE Direct Submission
 JOURNAL Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage ;
 BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
 - Web : www.genoscope.cns.fr)
 COMMENT Determination of this BAC-end sequence was carried out as part of a
 collaboration with the Berkeley Drosophila Genome Project (BDGP).
 The BDGP is constructing a physical map of the Drosophila
 melanogaster genome using these BACs. For further information
 please see http://www.fruitfly.org The BDGP Drosophila
 melanogaster BAC library was prepared by Kazutoyo Osoegawa and
 Aaron Mammeter in Pieter de Jong's Laboratory in the Department of
 Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
 NY. The library is named RPCI-98 and was constructed by partial
 EcoRI digestion of Drosophila DNA provided by the BDGP from the
 isogenic strain y2; cn bw sp, the same strain used for the BDGP's
 P1 and EST libraries. A more detailed description of the library
 and how to order individual BAC clones, the entire library, or
 filters for hybridization from the BACPAC Resource Center can be
 found at http://bacpac.med.buffalo.edu/drosophila.bac.htm.
 FEATURES
 source Location/Qualifiers
 1..910
 /organism="Drosophila melanogaster"
 /db_xref="taxon:7227"
 /clone_lib="RPCI-98"
 /clone="BACR14J71"
 /note="end : T7"
 BASE COUNT 202 a 63 c 112 g 198 t 335 others
 ORIGIN
 Query Match 4.6%; Score 40.8; DB 12; Length 910;
 Best Local Similarity 14.3%; Pred. No. 3;
 Matches 45; Conservative 143; Mismatches 126; Indels 0; Gaps 0;
 QY 321 ctggacacagctgacgaagcgttgacgaagcgcgcgtctgttcatacgcgcga 380
 ||:::|||||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
 Db 870 CRSSVCAAMGAS 811
 QY 381 catcgacgctacgattggcgcgcgcacatcagcgcgcgcgcgcgcgcgcgcgcgc 440
 ||:::|||||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
 Db 810 VSSVGSASRSASVSSSSSAGSAVSAVMAACSMVAASVAVASVAVARAKSKSA 751
 QY 441 cgcacgtacagcgcgcgaatcaagcgaatagcaaatatcatcagcgcgcgcgcgcgc 500
 ||:::|||||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
 Db 750 SNAKVAAYVARASAAVAVASAAVAVASVAVASVAVASVAVASVAVASVAVASV 691
 QY 501 ggcgcgcgaagcaaacacgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 560
 ||:::|||||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
 Db 690 SSSASASAMVWCRSAVSVASAAASAKRSASRSASVAAVAAVSSSVSSGSSVSC 631
 QY 561 cctgc 620
 ||:::|||||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
 Db 630 SSKRCGCSAS 571
 QY 621 cgc 634
 ||:::|||||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
 Db 570 CGSS 557
 RESULT 5
 LOCUS CNS004NB 839 bp DNA linear GSS 03-JUN-1999
 DEFINITION Drosophila melanogaster genome survey sequence TET3 end of BAC #
 BACR10E16 of RPCI-98 library from Drosophila melanogaster (fruit
 fly), genomic survey sequence.

Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: rstraus@rockefeller.edu

Contact: Robert Strausberg, Ph.D.
Email: cgaps-r@mail.nih.gov
Tissue Procurement: Christopher Moskalko, M.D., Ph.D., Michael R. Emmert-buck, M.D., Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution, information can be found through the I.M.A.G.E. www-bio.lnl.gov/bbrp/image/image.html
Insert length: 1939 Std Error: 0.00
Seq primer: -40UP from Glibco
High quality sequence strip: 437.

1.448

```

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2156779"
/clone_1ib="NC1_CGAP_Col4"
/issue_type="moderately-differentiated adenocarcinoma"
/lab_host="DH10B"
/note="Organ: colon; Vector: pCMV-SPORT6; Site_1: SalI;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT
Average insert size 1.7 Kb. Life Technologies catalog #:
11531-019"

```

4.3%; Score 40; DB 9; Length 448;
58: Pred NO 3 5.

[illegible]

Accession	Length	Type	Source	EST
AF016947	454 bp	mRNA	linear	EST 27-AUG-1998
U027e01.x1		Soares_NFL_T	GBC_S1 Homo sapiens CDNA clone	

IMAGE:1627512 3' similar to TR:O35260 O35260 NAC-1 PROTEIN. ;, mRNA sequence.

human.

ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
1 (bases 1 to 454)

National Cancer Institute, Cancer Genome Ana

Contact: Robert Strausberg, Ph.D.

Email: cgabbs-r@mail.nih.gov
This clone is available royalty-free through LENT; contact the IMaGE Consortium (Info@image.llnl.gov) for further information.
Insert length: 957 Std Error: 0.00
Seq primer: -40m13 fwd. ET from Amersham
High quality sequence: 241.

1.454

```
/organism="Homo sapiens"  
/db_xref="taxon:9606"  
/clone="IMAGE:1627512"
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64 a	144 c	166 g	80 f
------	-------	-------	------

[illegible]

BF940160	489 bp	mrna	linear	EST 22-JAN-2001
7043a05.x1		NCI_CGAP_Kid11 Homo sapiens CDNA clone	IMAGE:3576848 3'	

similar to TR:035260 035260 NAC-1 PROTEIN. ; mRNA sequence
BF940160

Homo sapiens

REFERENCE
1 (bases 1 to 489)
Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

Unpublished (1997)
Contact: Robert Strausberg, Ph.D.

Email: cgabbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LNL, send email to: info@image.llnl.gov
Seq primer: -40UP from Gibco.

1.489

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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3576848"
/clone_lib="NCI CGAP_Kid11"
/lab_host="DH10B"
/note="Organ: Kidney; Vector: pUT73D-Pac (Pharmacia) with
a modified polylinker; Site.1: Not I; Site.2: Eco RI;
Plasmid DNA from the normalized library NCI CGAP Kid3 was
prepared, and ss circles were made in vitro. Following RAP
purification, this DNA was used as tracer in a subtractive
hybridization reaction. The driver was PCR-amplified cDNAs
from a pool of 5,000 clones made from the same library

```


FEATURES
SOURCE

Query Match	4.5%;	Score 39.8;	DB 9;	Length 643;
Best Local Similarity	46.8%;	Pred. No. 4.8;		
Matches 125; Conservative	0;	Mismatches 142;	Indels 0;	Gaps 0

FEATURES	source
RESULT 16	
BI960503/c	
LOCUS	
DEFINITION	BI960503 653 bp mRNA linear EST 22-OCT-2001
ACCESSION	HVSMEN0024N07f Hordeum vulgare rachis EST library HVCdNA0015
VERSION	(normal) Hordeum vulgare cDNA clone HVSMEN0024N07f, mRNA sequence.
KEYWORDS	BI960503
SOURCE	BI960503.1 GI:16311758
ORGANISM	EST.
	barley.
	Hordeum vulgare
	Eutaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae
	; Triticeae; Hordeum.
REFERENCE	1 (bases 1 to 653)
AUTHORS	Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Chin,A., Begum,D.,
	Frish,D., Atkins,M., Yu,Y., Henry,D., Palmer,M., Rambo,T., Simmons,
	J., Oates,R. and Main,D.
	Development of a genetically and physically anchored EST resource
	for barley genomes. Morex rachis cDNA library
	unpublished (2001)
TITLE	Contact: Wing RA
JOURNAL	Clemson University Genomics Institute
COMMENT	Clemson University
	100 Jordan Hall, Clemson, SC 29634, USA
	Tel: 864 656 7288
	Fax: 864 656 4293
	Email: rwing@clemson.edu
	Total hg bases = 527
	Seq primer: AATTACCTCCTCAAGAAGG
	High quality sequence stop: 647.
	Location/Qualifiers
	1..653

Query Match	4.5%;	Score 39.8;	DB 10;	Length 653;
Best Local Similarity	45.2%;	Pred. No. 4.8;		
Matches 146;	Conservative 0;	Mismatches 177;	Indels 0;	Gaps 0;

487 caggcgggcagggtgctgcggcacaagcacaacgcgcgccacgcgcatacaagggtcaaa 546

RESULT 24
BF839785 452 bp mRNA linear EST 13-JAN-2001
LOCUS RC3-HT01007-281100-011-c02 HT01007 Homo sapiens cDNA, mRNA
DEFINITION
ACCESSION BF839785
VERSION BF839785.1 GI:12192184
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H., Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J., and Simpson, A.J.
TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE 20202663
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL:
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=RC3&t2=RC3-HT01007-281100-011-c02&t3=2000-11-28&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 452.
Location/Qualifiers
1..452
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="HT01007"
/dev_stage="Adult"
/note="Organ: head_neck; Vector: puc18; site_1: Smal; site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
BASE COUNT 119 a 128 c 131 g 74 t
ORIGIN
Query Match 4.3%; Score 38.6; DB 10; Length 452;
Best Local Similarity 47.3%; Pred. No. 8.8;
Matches 116; Conservative 0; Mismatches 129; Indels 0; Gaps 0;

QY 557 aggcc 561
Db 248 AGACC 252
RESULT 25
BE496100 494 bp mRNA linear EST 02-AUG-2000
LOCUS WHE1261.D06.H11ZS Secale cereale anther cDNA library Secale cereale
DEFINITION
ACCESSION BE496100
VERSION BE496100
KEYWORDS EST.
SOURCE Secale cereale
ORGANISM Secale cereale
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae
REFERENCE
AUTHORS Anderson, O.D., Butler, E., Chao, S., Choi, D.W., Close, T.J., Fenton, R.D., Gustafson, J.P., Han, P.S., Heila, C.C., Kang, Y., Lazo, G.R., Miller, R., Rausch, C.J., Ross, K., Seaton, C.L. and Tong, J.C.
TITLE The structure and function of the expressed portion of the wheat genomes - Anther cDNA library from rye
JOURNAL Unpublished (2000)
COMMENT Contact: Olin Anderson
US Department of Agriculture, Agriculture Research Service, Pacific West Area, Western Regional Research Center
800 Buchanan Street, Albany, CA 94710, USA
Tel: 5105595773
Fax: 5105593618
Email: oanderson@pw.usda.gov
Sequence have been trimmed to remove vector sequence and low quality sequence with phred score less than 20
Seq primer: Stragene SK primer.
Location/Qualifiers
1..494
/organism="Secale cereale"
/cultivar="Blanco"
/db_xref="taxon:4550"
/clone="WHE1261.D06.H11"
/clone_lib="Secale cereale anther cDNA library"
/dev_stage="Anther"
/tissue_type="Anther"
/lab_host="E. coli SOLR"
/note="Vector: Lambda uni-ZAP XR, excised phagemid; Site_1: EcoRI; Site_2: XhoI; Plants were grown in the greenhouse. Anthers were harvested and pooled from early meiosis to late meiosis. The tissue, total RNA, and poly(A) RNA were prepared (Butler, Ross and Gustafson) at University of Missouri, Columbia. A cDNA library was made, and the cDNA clones were in vivo excised to give plasmid DNA preparations and DNA sequencing were performed in the OD Anderson lab (all other authors)."
BASE COUNT 85 a 168 c 163 g 78 t
ORIGIN
Query Match 4.3%; Score 38.6; DB 10; Length 494;
Best Local Similarity 55.6%; Pred. No. 9.1;
Matches 74; Conservative 0; Mismatches 59; Indels 0; Gaps 0;

OY 811 gtgttaaccgca 823
 DB 341 GAGGCGAACGGCA 353
 RESULT 26
 BEA71037/c
 LOCUS
 DEFINITION BEA71037 502 bp mRNA linear EST 28-JUL-2000
 WHE0283_F10_K1925 Wheat drought-stressed seedling cDNA library
 Triticum aestivum CDNA clone WHE0283_F10_K19, mRNA sequence.
 ACCESSION BEA71037
 VERSION
 KEYWORDS
 SOURCE EST
 ORGANISM bread wheat.
 Triticum aestivum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae
 ; Triticaceae; Triticum.
 1 (bases 1 to 502)
 REFERENCE
 AUTHORS Anderson, O.D., Chao, S., Choi, D.W., Close, T.J., Fenton, R.D., Han
 , P.S., Hsia, C.C., Kang, Y., Lazo, G.R., Miller, R., Rausch, C.J.,
 Seaton, C.L. and Tong, J.C.
 The structure and function of the expressed portion of the wheat
 genomes - Drought-stressed seedling cDNA library
 Unpublished (2000)
 JOURNAL
 COMMENT Contact: Olin Anderson
 US Department of Agriculture, Agriculture Research Service, Pacific
 West Area, Western Regional Research Center
 800 Buchanan Street, Albany, CA 94710, USA
 Tel: 5105595773
 Fax: 5105595818
 Email: oanderson@pw.usda.gov
 Sequence have been trimmed to remove vector sequence and low
 quality sequence with phred score less than 20
 Seq primer: StrataGene SK primer.
 FEATURES
 source
 1. 502
 /organism="Triticum aestivum"
 /cultivar="Chinese Spring"
 /db_xref="taxon:4565"
 /clone="WHE0283_F10_K19"
 /clone_lib="Wheat drought-stressed seedling cDNA library"
 /tissue_type="Seedling without endosperm"
 /dev_stage="Five day old seedling"
 /lab_host="E. coli SOLR"
 /note="Vector: Lambda Uni-ZAP XR, excised phagemid;
 Site_1: EcoRI; Site_2: XhoI; Seeds were surface-sterilized
 , germinated and grown aseptically in the dark at room
 temperature on filter paper with water, nystatin and
 cefotaxime in covered crystallization dishes. Five-day old
 seedlings were incubated for one day at 90% RH. After
 removing endosperm, seedlings were transferred to
 desiccator jar containing saturated MgSO4 at room
 temperature for 24 hr. The tissue, total RNA, and poly(A)
 RNA were prepared, a cDNA library was made, and the cDNA
 clones were in vivo excised to give plasmid phagemids
 in the T7 Close lab (Choi, Close, Fenton) at the
 University of California, Riverside. Plasmid DNA
 preparations and DNA sequencing were performed in the OD
 Anderson lab (all other authors)."
 BASE COUNT 88 a 178 c 164 g 72 t
 ORIGIN
 Query Match 4.3%; Score 38.6; DB 10; Length 502;
 Best Local Similarity 44.9%; Pred. No. 9.2;
 Matches 146; Conservative 0; Mismatches 179; Indels 0; Gaps 0;
 OY 487 caggcgagcggtgcgagcaaaacccgcccgcgcatacaagggtcaaa 546
 DB 404 CATCGGAGCGCGCGCTTCCGCTGAGATCGACCGCTACTCCGATGTCGGCGCGGCAT 345
 OY 547 caatcatcaaggcctctgcgagcgagcaaccatcatctctccgacacagtcct 606

DB 344 CAGCCGCTTGTCCTCTGGAGAGTGGCGAGACGACGCTGCGCGCGCTACCCCAT 285
 OY 607 tctccgaggaagcgcggtgtggtggtatlttctcgcaaacctgataccatg 666
 DB 284 GGGCAGCGCGAACCCTGTCGGGAGCCACGCGCATGTGCGCGCATCTGCGCGCG 225
 OY 667 acactggtgcgaatgtgcaacgtcaagcggtgaacccgttctgtcgaa 726
 DB 224 GCGCAGCGGTGTGACGCGGACAGGTCTAGTGGCCATCACCACCTTGACGCGCGGTG 165
 OY 727 cgcctgcgagcgagcaggtctgtgtgacatccgcccgcgaagggaattgaac 786
 DB 164 CGGCTCTTGACGACACTGCGGTGTCAGACCTCCCTCGGTGCGCGGTACTGCAC 105
 OY 787 ggcacaaagccacagatgcgcg 811
 DB 104 GAGCAGCGCGCAGACGTCGCGCGTG 80
 RESULT 27
 BG904253/c
 LOCUS
 DEFINITION BG904253 545 bp mRNA linear EST 05-JUN-2001
 Tair1130F07R Tair1 Triticum aestivum CDNA clone Tair1130F07 5',
 mRNA sequence.
 ACCESSION BG904253
 VERSION
 KEYWORDS BG904253.1 GI:14311929
 EST.
 SOURCE bread wheat.
 ORGANISM Triticum aestivum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae
 ; Triticaceae; Triticum.
 1 (bases 1 to 545)
 REFERENCE
 AUTHORS Cloutier, S., Dong, G. and Walsh, A.
 JOURNAL
 COMMENT Wheat functional genomics - Thatcher Lr1 cDNA library
 Unpublished (2001)
 Contact: Dr. Sylvie Cloutier
 Cereal Research Centre, Agriculture and Agri-food Canada
 195 Dufferin Rd, Winnipeg, MB, Canada R3T 2M9
 Tel: (204) 983-2340
 Fax: (204) 983-4604
 Email: scloutier@em.agr.ca
 was cloned directionally, not all sequences generated with reverse
 primer were from the 5' end (same with forward primer and 3' end).
 Average insert size is >2.2 kb
 Plate: 130 row: F column: 07
 Seq primer: M13 Reverse.
 FEATURES
 source
 1. 545
 /organism="Triticum aestivum"
 /cultivar="Thatcher Lr1"
 /db_xref="taxon:4565"
 /clone="Tair1130F07"
 /clone_lib="Tair1"
 /tissue_type="leaf tissue"
 /dev_stage="14 Days old"
 /lab_host="E. coli XL0R"
 /note="Vector: Lambda ZapII; mass excised in plasmid
 vector PBK-CMV (Stratagene).; Site_1: EcoRI; Site_2: XhoI;
 mRNA obtained from wheat NIL Thatcher Lr1 24 hours after
 inoculation with leaf rust pathogen Puccinia triticina
 race BBB carrying the avirulence gene Avr1."
 BASE COUNT 96 a 190 c 178 g 81 t
 ORIGIN
 Query Match 4.3%; Score 38.6; DB 10; Length 545;
 Best Local Similarity 44.9%; Pred. No. 9.5;
 Matches 146; Conservative 0; Mismatches 179; Indels 0; Gaps 0;
 OY 487 caggcgagcggtgcgagcaaaacccgcccgcgcatacaagggtcaaa 546

D	b		422	CATCGAGAGCCGGGCTTGCCGTGGAAATGCACGCTACTCCTGGATGATGTCGGCCGGGCAT	363
OY		547	caaatcatcaagaagccctgcgcygcgycgagcgaagcaacatcatcctcgcccgaccacgttcct	606	
D	b	362	CAGCGCGTGTGACTCTCTGGAGGTGGCCAGGAACCAAGCTGGCGGGCCGCTACCCAT	303	
OY		607	tctccgcagaagaagcgcgcgctgtlbggcgagatttttctcgcgaacaactgcatacaacatg	666	
D	b	302	GGGCACGCCGAAACCGTTGCGGGGAACCCACGAGCATGTTCGGCGCCAATCTGCCCCGGCG	243	
OY		667	acactcgcgcgcaaaattgcacacgttaaaagcgcggaaacctgcpttttctcgtcgcgaa	726	
D	b	242	GCGGAGCGTGTGTGACCGCGAGAGGTCTAGTGCCATTCACCACATTGAGCGCTGCGGCTG	183	
OY		727	cgcctgcgccgcagcgaagaagcttgctgtttgcacatccgcocccgtccaaggggaaattgaac	786	
D	b	182	CGCGCTCTTTGACAGACTCGGCGTAATCCAGCACCCTCCCTCGGTGCGCGGGTACTGTGAC	123	
OY		787	ggcaacaaagcccacgatgcgcgcg	811	
D	b	122	GAGCACGCCGCGAGACGTGCGCCGCTG	98	

RESULT	28			
CNS015XR/C				
LOCUS	CNS015XR	1159 bp	DNA	linear
DEFINITION	Drosophila melanogaster genome survey sequence 17 of BAC Drosophila melanogaster / fruit			

ACCESSION	AL106041
VERSION	AL106041.1
	GI:5619746

ORGANISM

REFERENCE 1 (bases 1 to 1159)

TITLE	Direct Submission
JOURNAL	Genoscope - Centre National de Sequencage
Submitted (23-JUL-1999)	Submitted (23-JUL-1999)

COMMENT

COMMENT
determination of this BAC-end sequence was carried out as part of collaboration with the European Drosophila Genome Project (EDGP) - <http://www.edgp.ebi.ac.uk> . This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEHD (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector pBeloBAC11.

FEATURES	Location/Qualifiers
source	1. .1159

```

/organism="Drosophila melanogaster"
/plasmid="pBel0BAC11"
/db_xref="taxon:7227"
/clone_11b="DrosBAC"
/clone="BACN15017"
/notes="end : 17 g 178 t 490 others
BASE COUNT 448 a 36 c 7 g 178 t 490 others

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Query Match	4.38	Score	38.6	DB	12	Length	1159
Best Local Similarity	14.48	Pred. No.	13				
Matches	58	Conservative	179	Mismatches	167	Indels	0
						Gaps	0

QY 278 aaaacccggaagacatcgaaacaatggttccaaagcgtgtcacagctgtggaaacacgctgacg 337

Db 1128 ASASASSSSSSSSSASSSSMMAAAAGVVVASASARSASAAVSASVSVASVSVASVSV 106

QY 338 agagcttggacaagaagcgagcgctgctgttcatacgcgcgaatcgacatgcacatc 397

Db	1068	AVYASSASAAAARSAAGVAVVVAALVAAVMAAAMASASASASAAVSASVSAVYASMAS	1003
Qy	398	tgggcggagcgtacataccaagcaagcttcgtccactgcgcgcgcatgataccgc	457
Db	1008	MASASASASACASCAVMAVVVSVSSASVSSSSVSSSSASCRMSACASASASVCM	949
Qy	458	cgaatccaagcatagacaaaatcatcggaagcgggcaggtgctgcgcgcaaaagcaaa	517
Db	948	SASMSASGASVVSASASAAASASASASASASASASASASASASASVMSASMVHSAV	889
Qy	518	ccgcgcgcacccgagatcaaggggtcaacaagaatcatcaagcgcgcgcgcgcgcgaag	577
Db	888	VVVVSAVSASVSSASASVSMRVARVAAVGSASASASAMABASIAVTVVSSASASASMGASVS	829
Qy	578	caacatcatcctccgcgcacacgctccctctccgcagaagcgcgcgctgtgtggcgg	637
Db	828	AASSSVASASGSAATTASATVAAAMSMVAVRVAASMSRHAHSRVAVASASVSAVSSAVV	769
Qy	638	atttttcgcaaacctgcgcataccatcgcacctgcgcgcgaana	681
Db	768	AASATTTATVMAVASHMHTBAKCAAMVMSITVTRNBSVVSASARMA	725

Db 768 AASAWTTTATWVVASMHTBAKCMVWSTSYRTNBSSVSASAKMA / 23

RESULT 29

LOCUS	AM083767	318 bp	mRNA	linear	EST_14-OCF-1999
DEFINITION	xc25d02.x1 NCI_CGAP-Co19 Homo sapiens cDNA clone IMAGE:2585283 3'				
FEATURES	mRNA sequence.				

ACCESSION	AM083767	GI
VERSION	AM083767.1	GI
KEYWORDS	EST.	

FILE

Journal
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgaabs-r@mail.nih.gov

R. Emmert-Buck, M.D., Ph.D. CDNA library repository: www.cdna.library arrayed by: Christina Prange, The I.M.A.G.E. Consortium DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CCAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/dbfp/image/image.html
 Seq primer: -40UP from Gibco
 High quality sequence stop: 311.

high quality sequence deep	
Location/Qualifiers	
1. .318	
FEATURES	
source	

```
source
1.318
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2585283"
/clone_lib="NCI-CGAP_Col19"
/tissue_type="moderately differentiated adenocarcinoma"
/lab_host="DH10B"
/notes="Organ: colon; Vector: pCMV-SPORT6; Site:1; Salt:
```

	BASE COUNT	ORIGIN	Normalized version of "by life technologies."
36	a	112 c	126 g
44	t		

Query Match 4.3%; Score 38.4; DB 9; Length 318;
Best Local Similarity 60.6%; Pred. No. 8.6;
Matches 63; Conservative 0; Mismatches 41; Indels 0; Gaps 0

QY 490 gcggcaggggtgcgcgcaaaagcaaacgcgcgccacgcgcatacaagggtcaaca 549
 Db 306 GCCCCAGCGTCCCTCGACCCGAGGTCCGCCGCCGCCGACACAGGTTCGAGCA 247
 QY 550 atcatcaaggccctgcgcgcggcgaggaacacatcatctgcc 593
 Db 246 CGCATCTACGCCGAGCGGGGCGACGCCGCCACCATCTGTGC 203

RESULT 30
 LOCUS AI336998/c 487 bp mRNA linear EST 15-FEB-1999
 DEFINITION qx87e10.x1 NCI-CGAP.GC6 Homo sapiens cDNA clone IMAGE:2009514 3'
 similar to contains MER22.D3 TAR1 repetitive element ;, mRNA
 sequence.
 ACCESSION AI336998
 VERSION AI336998
 KEYWORDS GI:4073925
 SOURCE EST.
 ORGANISM human.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 487)
 AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 JOURNAL Unpublished (1997)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgaps-remail.nih.gov
 Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
 R. Emmert-Buck, M.D., Ph.D.
 cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
 Bonaudo, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 www-bio.llnl.gov/bbrp/image/html
 Insert length: 640 Std Error: 0.00
 Seq primer: -40UP from Gldco
 High quality sequence stop: 458.
 Location/Qualifiers
 1. 487

FEATURES
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 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_image="2009514"
 /clone_id="NCI-CGAP.GC6"
 /tissue_type="pooled germ cell tumors"
 /lab_host="DH10B"
 /note="Vector: pT7/3D-Pac (Pharmacia) with a modified
 from the normalized library NCI-CGAP.GC4 was prepared, and
 ss circles were made in vitro. Following HAP purification,
 this DNA was used as tracer in a subtractive hybridization
 reaction. The driver was PCR-amplified cDNAs from a pool
 of 5,000 clones made from the same library (clonoids
 1257096-1258631, 1469064-1470983, and 1475592-1476743).
 Subtraction by Bento Soares and M. Fatima Bonaudo."
 BASE COUNT 67 a 163 c 175 g 82 t
 ORIGIN

Query Match 4.3%; Score 38.4; DB 9; Length 487;
 Best Local Similarity 60.6%; Pred. No. 10;
 Matches 63; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

QY 490 gcggcaggggtgcgcgcaaaagcaaacgcgcgccacgcgcatacaagggtcaaca 549
 Db 287 GCCCCAGCGTCCCTCGACCCGAGGTCCGCCGCCGCCGACACAGGTTCGAGCA 228
 QY 550 atcatcaaggccctgcgcgcggcgaggaacacatcatctgcc 593
 Db 227 CGCATCTACGCCGAGCGGGGCGACGCCGCCACCATCTGTGC 184

RESULT 31
 LOCUS AM594194/c 498 bp mRNA linear EST 22-MAR-2000
 DEFINITION hg62a01.x1 NCI-CGAP.GC6 Homo sapiens cDNA clone IMAGE:2950152 3'
 similar to TR:035260 035260 NAC-1 PROTEIN.;, mRNA sequence.
 ACCESSION AM594194
 VERSION AM594194
 KEYWORDS GI:7281375
 SOURCE EST.
 ORGANISM human.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 498)
 AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 JOURNAL Unpublished (1997)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgaps-remail.nih.gov
 Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
 R. Emmert-Buck, M.D., Ph.D.
 cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
 Bonaudo, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 image.llnl.gov/image/html/iresources.shtml
 Possible reversed clone: polyT not found
 Seq primer: -40UP from Gldco
 High quality sequence stop: 297.
 Location/Qualifiers
 1. 498

FEATURES
 source
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_image="2950152"
 /clone_id="NCI-CGAP.GC6"
 /tissue_type="pooled germ cell tumors"
 /lab_host="DH10B"
 /note="Vector: pT7/3D-Pac (Pharmacia) with a modified
 from the normalized library NCI-CGAP.GC4 was prepared, and
 ss circles were made in vitro. Following HAP purification,
 this DNA was used as tracer in a subtractive hybridization
 reaction. The driver was PCR-amplified cDNAs from a pool
 of 5,000 clones made from the same library (clonoids
 1257096-1258631, 1469064-1470983, and 1475592-1476743).
 Subtraction by Bento Soares and M. Fatima Bonaudo."
 BASE COUNT 72 a 166 c 176 g 84 t
 ORIGIN

Query Match 4.3%; Score 38.4; DB 9; Length 498;
 Best Local Similarity 60.6%; Pred. No. 10;
 Matches 63; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

QY 490 gcggcaggggtgcgcgcaaaagcaaacgcgcgccacgcgcatacaagggtcaaca 549
 Db 303 GCCCCAGCGTCCCTCGACCCGAGGTCCGCCGCCGCCGACACAGGTTCGAGCA 244
 QY 550 atcatcaaggccctgcgcgcggcgaggaacacatcatctgcc 593
 Db 243 CGCATCTACGCCGAGCGGGGCGACGCCGCCACCATCTGTGC 200

RESULT 32
 LOCUS AM237064/c 546 bp mRNA linear EST 13-DEC-1999
 DEFINITION xm52g02.x1 NCI-CGAP.GC6 Homo sapiens cDNA clone IMAGE:2687858 3'
 similar to TR:035260 035260 NAC-1 PROTEIN.; contains PTRS.D1 TAR1

conditions (0, 12hr, 24hr) see Melis et al., (2000) Plant Phys. 122: 127-135; TAP + H2O2 (1, 12, 24 hr); TAP + sorbitol (1, 2, 6, 24 hr); TAP + Cd (1, 2, 6, 24 hr). PolyA mRNA was purified from each sample, pooled and cDNA synthesized. The cDNA was directionally cloned into lambda Zap II (Stratagene) in the EcoRI (5') and XhoI (3') sites. pBluescript II SK- plasmids were excised from the lambda Zap clones by superinfection with Exsist (Stratagene) phage. The library was normalized using method 4 described in Bonaldo et al., (1996) Genome Research 6: 791-806."

BASE COUNT 72 a 140 c 133 g 61 t

ORIGIN

Query Match 4.3%; Score 38.2; DB 10; Length 406;
Best Local Similarity 55.7%; Pred. No. 11;
Matches 73; Conservative 0; Mismatches 58; Indels 0; Gaps 0;

OY 428 cgttccacctgacccgcatgtacacgagcgcggaatacaagcgtatagacaatcatgc 487
DB 88 CGCTCAACATGCGCGGCTCTACACAGCTGCGCCACATCTTCTGCGGAGAACACCTCT 147
OY 488 aggcggaggggtgctgcggcgaagcaaacgcgcgcacccgcgtacatacaagggtcaaac 547
DB 148 GGGCGCATGGCATGAGCCACCTCGCGCCAGCCAGCACCGCGCGGAGACGCCGC 207
OY 548 aaatcatcaag 558
DB 208 ACATCTACAG 218

RESULT 37 499 bp mRNA linear EST 19-SEP-2001
LOCUS B1723630
DEFINITION 1031067006.y2 C. reinhardtii CC-1690, Stress II (normalized),
Lambda Zap II Chlamydomonas reinhardtii cDNA, mRNA sequence.
B1723630
B1723630.1 GI:15699325
ACCESSION
VERSION B1723630.1
KEYWORDS EST.
SOURCE Chlamydomonas reinhardtii.
ORGANISM Chlamydomonas reinhardtii.
REFERENCE Grossman, A., Chang, C.-W., Davies, J., Harris, E., Hauser, C., Lefebvre, P., McDermott, J.P., Shrager, J., Silflow, C., and Stern, D.,
Analyses of the Chlamydomonas reinhardtii Genome: A Model,
Unicellular System for Analyzing Gene Function and Regulation in
Vascular Plants. Project: 1031
Unpublished (2001)
JOURNAL Contact: Charles Hauser
COMMENT DCMB Box 91000
Duke University
Durham, NC 27708-1000
Tel: 919 613 8159
Fax: 919 613 8177
Email: chauser@duke.edu.

FEATURES
source Location/Qualifiers

1. 499
/organism="Chlamydomonas reinhardtii"
/strain="CC-1690 wild type mt+ 21gr"
/db_xref="taxon:3055"
/clone_lib="C. reinhardtii CC-1690, Stress II (normalized),
Lambda Zap II"
/note="Vector: pBluescript II SK-, Site.1: EcoRI; Site.2:
XhoI; Stress condition II library, constructed by John
Davies and Jeffrey McDermott, combines cDNAs from CC-1690
cells grown to mid-log phase in TAP (NH4+ - containing)
and shifted to TAP - NO3- (24hrs); H2 production
conditions (0, 12hr, 24hr) see Melis et al., (2000) Plant
Phys. 122: 127-135; TAP + H2O2 (1, 12, 24 hr); TAP +
sorbitol (1, 2, 6, 24 hr); TAP + Cd (1, 2, 6, 24 hr).

PolyA mRNA was purified from each sample, pooled and cDNA synthesized. The cDNA was directionally cloned into lambda Zap II (Stratagene) in the EcoRI (5') and XhoI (3') sites. pBluescript II SK- plasmids were excised from the lambda Zap clones by superinfection with Exsist (Stratagene) phage. The library was normalized using method 4 described in Bonaldo et al., (1996) Genome Research 6: 791-806."

BASE COUNT 94 a 169 c 162 g 74 t

ORIGIN

Query Match 4.3%; Score 38.2; DB 10; Length 499;
Best Local Similarity 55.7%; Pred. No. 12;
Matches 73; Conservative 0; Mismatches 58; Indels 0; Gaps 0;

OY 428 cgttccacctgacccgcatgtacacgagcgcggaatacaagcgtatagacaatcatgc 487
DB 88 CGCTCAACATGCGCGGCTCTACACAGCTGCGCCACATCTTCTGCGGAGAACACCTCT 147
OY 488 aggcggaggggtgctgcggcgaagcaaacgcgcgcacccgcgtacatacaagggtcaaac 547
DB 148 GGGCGCATGGCATGAGCCACCTCGCGCCAGCCAGCACCGCGCGGAGACGCCGC 207
OY 548 aaatcatcaag 558
DB 208 ACATCTACAG 218

RESULT 38 535 bp mRNA linear EST 19-SEP-2001
LOCUS B1724519
DEFINITION 1031072D08.y1 C. reinhardtii CC-1690, Stress II (normalized),
Lambda Zap II Chlamydomonas reinhardtii cDNA, mRNA sequence.
B1724519
B1724519.1 GI:15700214
ACCESSION
VERSION B1724519
KEYWORDS EST.
SOURCE Chlamydomonas reinhardtii.
ORGANISM Chlamydomonas reinhardtii.
REFERENCE Grossman, A., Chang, C.-W., Davies, J., Harris, E., Hauser, C., Lefebvre, P., McDermott, J.P., Shrager, J., Silflow, C., and Stern, D.,
Analyses of the Chlamydomonas reinhardtii Genome: A Model,
Unicellular System for Analyzing Gene Function and Regulation in
Vascular Plants. Project: 1031
Unpublished (2001)
JOURNAL Contact: Charles Hauser
COMMENT DCMB Box 91000
Duke University
Durham, NC 27708-1000
Tel: 919 613 8159
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Email: chauser@duke.edu.

FEATURES
source Location/Qualifiers

1. 535
/organism="Chlamydomonas reinhardtii"
/strain="CC-1690 wild type mt+ 21gr"
/db_xref="taxon:3055"
/clone_lib="C. reinhardtii CC-1690, Stress II (normalized),
Lambda Zap II"
/note="Vector: pBluescript II SK-, Site.1: EcoRI; Site.2:
XhoI; Stress condition II library, constructed by John
Davies and Jeffrey McDermott, combines cDNAs from CC-1690
cells grown to mid-log phase in TAP (NH4+ - containing)
and shifted to TAP - NO3- (24hrs); H2 production
conditions (0, 12hr, 24hr) see Melis et al., (2000) Plant
Phys. 122: 127-135; TAP + H2O2 (1, 12, 24 hr); TAP +
sorbitol (1, 2, 6, 24 hr); TAP + Cd (1, 2, 6, 24 hr).
PolyA mRNA was purified from each sample, pooled and cDNA
synthesized. The cDNA was directionally cloned into lambda
Zap II (Stratagene) in the EcoRI (5') and XhoI (3')

RESULT 45
PT537370

BI531370
LOCUS

LOCUS	535 bp	mRNA	linear	EST 29-AUG-2000
B1531370				
1024113C10.y1				
DEFINITION				
Chlamydomonas reinhardtii CC-1690, normalized, Lambda Zap II				
Chlamydomonas reinhardtii cDNA, mRNA sequence.				

ACCESSION BI531370

KEYWORDS EST.

SOURCE	ORGANISM	Chlamydomonas reinhardtii
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99	99	99
100	100	100

Eukariyota; Viridiplantae; Chlamydomonadaceae; Chlamy

REFERENCE	1 (bases 1 to 333)
AUTHORS	Grossman, A., Chang, C.-W., Davies, J., Harris, E., Hauser, C., Lefebvre

11. P., McDermott, J. P., Shrago, J., Sillow, C. and Stern, B.
Analyses of the Chlamydomonas reinhardtii Genome: A Model,
Title

Unicellular System for Analyzing Gene Function and Regulation in
Vascular Plants Project: 1024b

JOURNAL
unpublished (2001)

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Tel: 919 613 8135
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FEATURES
Email: chauser@duke.edu.
Location/Qualifiers

```
source
1. .535
/organism="Chlamydomonas reinhardtii"
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```
/strain="CC-1690 wild type mt+ 21gr"  
/ab.scf="taxon:3055"
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/clone_lib="C. reinhardtii CC-1690, normalized, Lambda Za
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27 /note="Vector: pBluescript II SK-; Site_1: EcoRI; Site_2:

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McDermott, combines cDNAs from CC-1690 cells grown to

mid-log phase in TAP (acetate-containing) medium in the light, TAP medium in the dark, HS (minimal) medium in

ambient levels of CO₂ and HS medium bubbled with 5% CO₂. PolvA mRNA was purified from each sample, pooled and cDNA

synthesized. The cDNA was directionally cloned into lambda phage vector (Stratagene) in the EcoRI (5') and XhoI (3') sites

pBluescript II SK- plasmids were excised from the lambda

phage. The library was normalized using method 4 described

BASE COUNT	94 a	173 c	175 g	93 t
IN DONALD	ec	ai	(1750)	SCHEMATIC

ORIGIN

4 38: score 38: NA 10: Length 535:

Query Match	4.38;	Score 38;	DB 10;	Length 535;
-------------	-------	-----------	--------	-------------

Matches	122;	Conservative	0;	Mismatches	140;	Indels	0;	Gaps	0;
---------	------	--------------	----	------------	------	--------	----	------	----

QY 344 tggacaaggcggaaggctgtgttcatacggccgcacatcggcagctacgattgggcg 403

Db 231 TGGCCAGGGAACGTGGCAGGTTCACACGCCGCACATCAGCAGATGAGCTGGCCC 290

404aacactacatcaagccaagcaacttcgaattccaactgaaccgcatgtacaaagccgcgaaaa 463

301 TATTCATCCTGACCTGCTCCACG 350
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523

[illegible][illegible][illegible]

Db 411 GCAAGTACGATGACCGTGTGAGGTTGACCTTTGACCGGTTCTGGGTTGACCTGGGCGCGG 370

QY 584 tcattctgcccgaaccacgtccc 605

Db 471 ATAGCCTGCGCGCGGACCTCCC 492

Search completed: June 29, 2002, 22:09:22
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